

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 10/083,620
Source: PIPE
Date Processed by STIC: 3/13/02

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

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1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
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OIPE

Errors on pp. 5

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/083,620

DATE: 03/13/2002
TIME: 15:12:14

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Output Set : N:\CRF3\03132002\J083620.raw

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3 <110> APPLICANT: Loughney, Kate
5 <120> TITLE OF INVENTION: Phosphodiesterase 10
7 <130> FILE REFERENCE: 27866/35308
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/083,620
C--> 10 <141> CURRENT FILING DATE: 2002-02-26
12 <150> PRIOR APPLICATION NUMBER: 60/075,508
13 <151> PRIOR FILING DATE: 1998-02-23
15 <160> NUMBER OF SEQ ID NOS: 26
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1548
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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31                               1                               5
33 aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta 100
34 Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu
35 10                               15                               20                               25
37 atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc 148
38 Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe
39                               30                               35                               40
41 aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta 196
42 Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu
43                               45                               50                               55
45 gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa 244
46 Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys
47                               60                               65                               70
49 tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc 292
50 Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser
51                               75                               80                               85
53 agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag 340
54 Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys
55 90                               95                               100                               105
57 aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc 388
58 Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu
59                               110                               115                               120
61 tct cca gag acc atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg 436
62 Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp

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Input Set : A:\Pdel10.app
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65	ctt tgg gag ccc aat gag atg ctg agc tgc ctg gag cac atg tac cac	484		
66	Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His			
67	140	145	150	
69	gac ctc ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctc agg	532		
70	Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg			
71	155	160	165	
73	agg tgg ctg ttc tgc gtc cac gac aac tac aga aac aac ccc ttc cac	580		
74	Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His			
75	170	175	180	185
77	aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc	628		
78	Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val			
79	190	195	200	
81	tgg ctc tgc agt ctc cag gag aag ttc tca caa acg gat atc ctg atc	676		
82	Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile			
83	205	210	215	
85	cta atg aca gcg gcc atc tgc cac gat ctg gac cat ccc gcc tac aac	724		
86	Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn			
87	220	225	230	
89	aac acg tac cag atc aat gcc cgc aca gag ctg gcg gtc cgc tac aat	772		
90	Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn			
91	235	240	245	
93	gac atc tca ccg ctg gag aac cac cac tgc gcc gtg gcc ttc cag atc	820		
94	Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile			
95	250	255	260	265
97	ctc gcc gag cct gag tgc aac atc ttc tcc aac atc cca cct gat ggg	868		
98	Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly			
99	270	275	280	
101	ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gac	916		
102	Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp			
103	285	290	295	
105	atg gca aga cat gca gaa att atg gat tct ttc aaa gag aaa atg gag	964		
106	Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu			
107	300	305	310	
109	aat ttt gac tac agc aac gag gag cac atg acc ctg ctg aag atg att	1012		
110	Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile			
111	315	320	325	
113	ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt cca atg gaa gtc	1060		
114	Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val			
115	330	335	340	345
117	gca gag cct tgg gtg gac tgt tta tta gag gaa tat ttt atg cag agc	1108		
118	Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser			
119	350	355	360	
121	gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga	1156		
122	Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg			
123	365	370	375	
125	gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc	1204		
126	Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val			
127	380	385	390	

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129 ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag 1252
130 Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu
131      395      400      405
133 gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag 1300
134 Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu
135 410      415      420      425
137 ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac 1348
138 Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp
139      430      435      440
141 agc ttg acg tct ggg gcc acc gag aag tcc aga ggg aga agc aga gat 1396
142 Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Gly Arg Ser Arg Asp
143      445      450      455
145 gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc ggggggcgtg 1443
146 Val Lys Asn Ser Glu Gly Asp Cys Ala
147      460      465
149 gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc 1503
151 ctgggcacct ggcaccacaa gaccatgttt tctaagaacc atttt 1548
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155 <211> LENGTH: 466
156 <212> TYPE: PRT
157 <213> ORGANISM: Homo sapiens
159 <400> SEQUENCE: 2
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161 1      5      10      15
163 Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln
164      20      25      30
166 Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala
167      35      40      45
169 Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu
170      50      55      60
172 Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys
173 65      70      75      80
175 Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys
176      85      90      95
178 Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp
179      100      105      110
181 Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala
182      115      120      125
184 Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met
185      130      135      140
187 Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp
188 145      150      155      160
190 Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His
191      165      170      175
193 Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys
194      180      185      190
196 Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu
197      195      200      205
199 Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/083,620

DATE: 03/13/2002

TIME: 15:12:15

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Output Set: N:\CRF3\03132002\J083620.raw

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200      210      215      220
202 His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala
203 225      230      235      240
205 Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn
206      245      250      255
208 His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn
209      260      265      270
211 Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly
212      275      280      285
214 Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile
215      290      295      300
217 Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu
218 305      310      315      320
220 Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile
221      325      330      335
223 Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys
224      340      345      350
226 Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly
227      355      360      365
229 Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr
230      370      375      380
232 Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr
233 385      390      395      400
235 Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu
236      405      410      415
238 Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala
239      420      425      430
241 Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr
242      435      440      445
244 Glu Lys Ser Arg Gly Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp
245      450      455      460
247 Cys Ala
248 465
251 <210> SEQ ID NO: 3
252 <211> LENGTH: 225
253 <212> TYPE: DNA
254 <213> ORGANISM: Homo sapiens
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Nucleotides at positions 130, 186, and 205 are
258     either A, T, G, or C.
260 <400> SEQUENCE: 3
261 agcgaccgtg agaagtcaga aggccttcoct gtggaaccgt tcatggaccg agacaaagtg 60
263 accaaggcca cagccagat tgggttcacg aagtttgccc tgatcccaat gtttgaaaca 120
W--> 265 gtgaccaagn tcttcccat ggttgaggag atcatgctgc agccacttg ggaatcccga 180
W--> 267 gatcgtacg aggagctgaa gcgntagat gacgccatga aagag 225
270 <210> SEQ ID NO: 4
271 <211> LENGTH: 158
272 <212> TYPE: DNA
273 <213> ORGANISM: Homo sapiens

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RAW SEQUENCE LISTING

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TIME: 15:12:15

Input Set : A:\Pdel0.app

Output Set: N:\CRF3\03132002\J083620.raw

275 <220> FEATURE:
 276 <223> OTHER INFORMATION: Nucleotides at positions 12, 36, 61, and 109 are
 277 either A, T, G, or C.
 279 <400> SEQUENCE: 4

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 W--> 282 gnaaccacca ctgcgccgtg gccttccaga tcctcgccga gcctgagtgn aacatcttct 120
 284 ccaacatccc acctgatggg ttcaagcaga tccgacag 158
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 288 <211> LENGTH: 98
 289 <212> TYPE: DNA
 290 <213> ORGANISM: Homo sapiens
 292 <220> FEATURE:
 293 <223> OTHER INFORMATION: Nucleotides at positions 14, 22, and 50 are either
 294 A, T, C, or G.
 296 <400> SEQUENCE: 5

W--> 297 gagaacacca ctgngccgtg gncttccaga tcctcgccga gcctgagtgn aacatcttct 60
 299 ccaacatccc acctgatggg ttcaagcaga tccgacag 98
 302 <210> SEQ ID NO: 6
 303 <211> LENGTH: 418
 304 <212> TYPE: DNA
 305 <213> ORGANISM: Homo sapiens
 307 <220> FEATURE:
 308 <223> OTHER INFORMATION: Nucleotides at positions 1, 267, 352, 400, and 411
 309 are either A, T, G, or C.
 311 <400> SEQUENCE: 6

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 314 gtctctaattg tcaactgtctg ctgcattccc tgcagagcga cctgagagaag tcagaaggcc 120
 316 ttcccggtggc cccgttcatg gaccgagaca aagtgaccaa ggccacagcc caggattggg 180
 318 ttcatcaag tttgtcctga tccaatgtt tgaaacagt accaagctct tccccatggg 240
 W--> 320 ttgagggaga ttcattgctg cagccanttt ggggaatccc gaggattcgc tacgagggag 300
 W--> 322 cttgaagcgg gattaggtg gacggccatg gaaaggagt ttacaggaag gnaggatttg 360
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 328 <211> LENGTH: 428
 329 <212> TYPE: DNA
 330 <213> ORGANISM: Homo sapiens
 332 <220> FEATURE:
 333 <223> OTHER INFORMATION: Nucleotides at positions 1, 82, 92, 130, 347, 390,
 334 and 396 are either A, T, G, or C.
 336 <400> SEQUENCE: 7

W--> 337 nagaataaag tgaacaaaat ggttcttaga aaacatggc ttgtggtgcc aggtgcccag 60
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 343 tctggacttc tgggtggccc cagacgtcaa gctgtcagtc ttcttctgta actctttcat 240
 345 gggcgatcat tatccgcttc agctcctcgt aggcgatctc ggggattccc aaagtgggct 300
 W--> 347 gcagcatgat ctctctcaac catggggggg aggagcttgg ggcaactngt ttcaaaaatt 360
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 354 <210> SEQ ID NO: 8

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/083,620

DATE: 03/13/2002

TIME: 15:12:16

Input Set : A:\Pd10.app

Output Set: N:\CRF3\03132002\J083620.raw

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:265 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:265 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/083,620

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Input Set : A:\Pdel0.app

Output Set: N:\CRF3\03132002\J083620.raw

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